

Stephen K Burley

List of Publications by Year in descending order

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245
papers

29,630
citations

6254

80
h-index

5539

163
g-index

261
all docs

261
docs citations

261
times ranked

30072
citing authors

#	ARTICLE	IF	CITATIONS
1	Co-crystal structure of the HNF-3/fork head DNA-recognition motif resembles histone H5. <i>Nature</i> , 1993, 364, 412-420.	27.8	1,253
2	Co-crystal structure of TBP recognizing the minor groove of a TATA element. <i>Nature</i> , 1993, 365, 520-527.	27.8	1,083
3	RCSB Protein Data Bank: biological macromolecular structures enabling research and education in fundamental biology, biomedicine, biotechnology and energy. <i>Nucleic Acids Research</i> , 2019, 47, D464-D474.	14.5	918
4	RCSB Protein Data Bank: powerful new tools for exploring 3D structures of biological macromolecules for basic and applied research and education in fundamental biology, biomedicine, biotechnology, bioengineering and energy sciences. <i>Nucleic Acids Research</i> , 2021, 49, D437-D451.	14.5	918
5	Protein production and purification. <i>Nature Methods</i> , 2008, 5, 135-146.	19.0	763
6	Recognition by Max of its cognate DNA through a dimeric b/HLH/Z domain. <i>Nature</i> , 1993, 363, 38-45.	27.8	727
7	Hierarchical phosphorylation of the translation inhibitor 4E-BP1. <i>Genes and Development</i> , 2001, 15, 2852-2864.	5.9	703
8	Protein Data Bank: the single global archive for 3D macromolecular structure data. <i>Nucleic Acids Research</i> , 2019, 47, D520-D528.	14.5	671
9	Cocrystal Structure of the Messenger RNA 5' Cap-Binding Protein (eIF4E) Bound to 7-methyl-GDP. <i>Cell</i> , 1997, 89, 951-961.	28.9	635
10	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D271-D281.	14.5	619
11	Protein Data Bank (PDB): The Single Global Macromolecular Structure Archive. <i>Methods in Molecular Biology</i> , 2017, 1607, 627-641.	0.9	592
12	Type VI secretion apparatus and phage tail-associated protein complexes share a common evolutionary origin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4154-4159.	7.1	576
13	Crystal structure of a TFIIB-TBP-TATA-element ternary complex. <i>Nature</i> , 1995, 377, 119-128.	27.8	543
14	A standard reference frame for the description of nucleic acid base-pair geometry 1 Edited by P. E. Wright 2 This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton... <i>Journal of Molecular Biology</i> , 2001, 313, 229-237.	4.2	533
15	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	17.5	520
16	Mol* Viewer: modern web app for 3D visualization and analysis of large biomolecular structures. <i>Nucleic Acids Research</i> , 2021, 49, W431-W437.	14.5	515
17	ModBase, a database of annotated comparative protein structure models, and associated resources. <i>Nucleic Acids Research</i> , 2011, 39, D465-D474.	14.5	506
18	Molecular basis of mouse microphthalmia (mi) mutations helps explain their developmental and phenotypic consequences. <i>Nature Genetics</i> , 1994, 8, 256-263.	21.4	505

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19	Winged helix proteins. <i>Current Opinion in Structural Biology</i> , 2000, 10, 110-116.	5.7	497
20	X-Ray Structures of Myc-Max and Mad-Max Recognizing DNA. <i>Cell</i> , 2003, 112, 193-205.	28.9	474
21	Recognition of Polyadenylate RNA by the Poly(A)-Binding Protein. <i>Cell</i> , 1999, 98, 835-845.	28.9	465
22	The RCSB Protein Data Bank: views of structural biology for basic and applied research and education. <i>Nucleic Acids Research</i> , 2015, 43, D345-D356.	14.5	461
23	Cap-Dependent Translation Initiation in Eukaryotes Is Regulated by a Molecular Mimic of eIF4G. <i>Molecular Cell</i> , 1999, 3, 707-716.	9.7	457
24	Crystal structure of TFIID TATA-box binding protein. <i>Nature</i> , 1992, 360, 40-46.	27.8	430
25	Structure of nucleotide-binding domain 1 of the cystic fibrosis transmembrane conductance regulator. <i>EMBO Journal</i> , 2004, 23, 282-293.	7.8	376
26	Structural genomics: beyond the Human Genome Project. <i>Nature Genetics</i> , 1999, 23, 151-157.	21.4	369
27	Biophysical Studies of eIF4E Cap-binding Protein: Recognition of mRNA 5' Cap Structure and Synthetic Fragments of eIF4G and 4E-BP1 Proteins. <i>Journal of Molecular Biology</i> , 2002, 319, 615-635.	4.2	353
28	Sequence-Specific RNA Binding by a Nova KH Domain. <i>Cell</i> , 2000, 100, 323-332.	28.9	307
29	Structure of the winged-helix protein hRFX1 reveals a new mode of DNA binding. <i>Nature</i> , 2000, 403, 916-921.	27.8	296
30	Crystal Structure of the MazE/MazF Complex. <i>Molecular Cell</i> , 2003, 11, 875-884.	9.7	271
31	Structural similarity between TAFs and the heterotetrameric core of the histone octamer. <i>Nature</i> , 1996, 380, 316-322.	27.8	251
32	Crystal Structure of a GCN5-Related N-acetyltransferase. <i>Cell</i> , 1998, 94, 439-449.	28.9	233
33	X-Ray Structures of the Universal Translation Initiation Factor IF2/eIF5B. <i>Cell</i> , 2000, 103, 781-792.	28.9	227
34	RCSB Protein Data Bank: Enabling biomedical research and drug discovery. <i>Protein Science</i> , 2020, 29, 52-65.	7.6	223
35	RCSB Protein Data Bank: Sustaining a living digital data resource that enables breakthroughs in scientific research and biomedical education. <i>Protein Science</i> , 2018, 27, 316-330.	7.6	219
36	Structure determination and refinement of bovine lens leucine aminopeptidase and its complex with bestatin. <i>Journal of Molecular Biology</i> , 1992, 224, 113-140.	4.2	215

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37	1.9 Å... resolution refined structure of TBP recognizing the minor groove of TATAAAAG. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 638-653.	8.2	212
38	Validation of Structures in the Protein Data Bank. <i>Structure</i> , 2017, 25, 1916-1927.	3.3	210
39	HDEA, a periplasmic protein that supports acid resistance in pathogenic enteric bacteria 1 Edited by P. E. Wright. <i>Journal of Molecular Biology</i> , 2000, 295, 605-612.	4.2	201
40	A Conserved HEAT Domain within eIF4G Directs Assembly of the Translation Initiation Machinery. <i>Molecular Cell</i> , 2001, 7, 193-203.	9.7	199
41	An overview of structural genomics. , 2000, 7, 932-934.		197
42	Translational Repression by a Novel Partner of Human Poly(A) Binding Protein, Paip2. <i>Molecular Cell</i> , 2001, 7, 205-216.	9.7	197
43	Total Chemical Synthesis of a Unique Transcription Factor-Related Protein: cMyc-Max. <i>Journal of the American Chemical Society</i> , 1995, 117, 2998-3007.	13.7	193
44	A Novel Peptide Recognition Mode Revealed by the X-Ray Structure of a Core U2AF35/U2AF65 Heterodimer. <i>Cell</i> , 2001, 106, 595-605.	28.9	192
45	A Modular Cross-Linking Approach for Exploring Protein Interactions. <i>Journal of the American Chemical Society</i> , 2003, 125, 2416-2425.	13.7	189
46	A histone octamer-like structure within TFIID. <i>Nature</i> , 1996, 380, 356-359.	27.8	184
47	A Novel Mode of Gleevec Binding Is Revealed by the Structure of Spleen Tyrosine Kinase. <i>Journal of Biological Chemistry</i> , 2004, 279, 55827-55832.	3.4	179
48	D3R grand challenge 2015: Evaluation of proteinâ€“ligand pose and affinity predictions. <i>Journal of Computer-Aided Molecular Design</i> , 2016, 30, 651-668.	2.9	178
49	The cholesterol-regulated StarD4 gene encodes a StAR-related lipid transfer protein with two closely related homologues, StarD5 and StarD6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6943-6948.	7.1	169
50	Structural genomics: A pipeline for providing structures for the biologist. <i>Protein Science</i> , 2002, 11, 723-738.	7.6	168
51	Outcome of the First wwPDB Hybrid/Integrative Methods Task Force Workshop. <i>Structure</i> , 2015, 23, 1156-1167.	3.3	159
52	Crystal structure of the <i>Mus musculus</i> cholesterol-regulated START protein 4 (StarD4) containing a StAR-related lipid transfer domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 6949-6954.	7.1	158
53	D3R Grand Challenge 2: blind prediction of proteinâ€“ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2018, 32, 1-20.	2.9	156
54	Mechanism of action of a flavin-containing monooxygenase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9832-9837.	7.1	152

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55	Probing the solution structure of the DNA-binding protein Max by a combination of proteolysis and mass spectrometry. <i>Protein Science</i> , 1995, 4, 1088-1099.	7.6	149
56	Structural genomics of protein phosphatases. <i>Journal of Structural and Functional Genomics</i> , 2007, 8, 121-140.	1.2	148
57	A public-private partnership to unlock the untargeted kinome. <i>Nature Chemical Biology</i> , 2013, 9, 3-6.	8.0	141
58	Crystal Structure of Negative Cofactor 2 Recognizing the TBP-DNA Transcription Complex. <i>Cell</i> , 2001, 106, 71-81.	28.9	134
59	Use of dynamic light scattering to assess crystallizability of macromolecules and macromolecular assemblies. <i>Structure</i> , 1994, 2, 357-359.	3.3	131
60	Structural bases for CRMP function in plexin-dependent semaphorin3A signaling. <i>EMBO Journal</i> , 2004, 23, 9-22.	7.8	130
61	OneDep: Unified wwPDB System for Deposition, Biocuration, and Validation of Macromolecular Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 536-545.	3.3	130
62	Architectural Transcription Factors: Proteins That-Remodel DNA. <i>Cell</i> , 1997, 88, 733-736.	28.9	126
63	Phosphorylation of eIF4E attenuates its interaction with mRNA 5' cap analogs by electrostatic repulsion: Intein-mediated protein ligation strategy to obtain phosphorylated protein. <i>Rna</i> , 2003, 9, 52-61.	3.5	124
64	Uncoupling of Initiation Factor eIF5B/IF2 GTPase and Translational Activities by Mutations that Lower Ribosome Affinity. <i>Cell</i> , 2002, 111, 1015-1025.	28.9	123
65	SGX523 is an exquisitely selective, ATP-competitive inhibitor of the MET receptor tyrosine kinase with antitumor activity <i>in vivo</i> . <i>Molecular Cancer Therapeutics</i> , 2009, 8, 3181-3190.	4.1	123
66	Co-crystal structure of sterol regulatory element binding protein 1a at 2.3 Å resolution. <i>Structure</i> , 1998, 6, 661-672.	3.3	122
67	Cloning and Characterization of 4EHP, a Novel Mammalian eIF4E-related Cap-binding Protein. <i>Journal of Biological Chemistry</i> , 1998, 273, 13104-13109.	3.4	122
68	Recognition of eIF4G by Rotavirus NSP3 Reveals a Basis for mRNA Circularization. <i>Molecular Cell</i> , 2002, 9, 1273-1283.	9.7	121
69	2.1 Å... resolution refined structure of a TATA box-binding protein (TBP). <i>Nature Structural and Molecular Biology</i> , 1994, 1, 621-637.	8.2	108
70	RCSB Protein Data Bank: Architectural Advances Towards Integrated Searching and Efficient Access to Macromolecular Structure Data from the PDB Archive. <i>Journal of Molecular Biology</i> , 2021, 433, 166704.	4.2	106
71	Exploration of disorder in protein structures by X-ray restrained molecular dynamics. <i>Proteins: Structure, Function and Bioinformatics</i> , 1991, 10, 340-358.	2.6	105
72	D3R Grand Challenge 3: blind prediction of protein-ligand poses and affinity rankings. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 1-18.	2.9	104

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73	Crystal structures of Nova-1 and Nova-2 K-homology RNA-binding domains. <i>Structure</i> , 1999, 7, 191-203.	3.3	103
74	A public database of macromolecular diffraction experiments. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 1181-1193.	2.3	103
75	Structural Basis for Autoinhibition and Mutational Activation of Eukaryotic Initiation Factor 2 [±] Protein Kinase GCN2*[boxes]. <i>Journal of Biological Chemistry</i> , 2005, 280, 29289-29299.	3.4	100
76	Recognition of the Rotavirus mRNA 3 [±] Consensus by an Asymmetric NSP3 Homodimer. <i>Cell</i> , 2002, 108, 71-81.	28.9	96
77	SOD1 Phosphorylation by mTORC1 Couples Nutrient Sensing and Redox Regulation. <i>Molecular Cell</i> , 2018, 70, 502-515.e8.	9.7	94
78	The RCSB PDB [±] Molecule of the Month [±] Inspiring a Molecular View of Biology. <i>PLoS Biology</i> , 2015, 13, e1002140.	5.6	88
79	The TATA box binding protein. <i>Current Opinion in Structural Biology</i> , 1996, 6, 69-75.	5.7	86
80	Physical and Functional Interaction between the Eukaryotic Orthologs of Prokaryotic Translation Initiation Factors IF1 and IF2. <i>Molecular and Cellular Biology</i> , 2000, 20, 7183-7191.	2.3	84
81	SGX393 inhibits the CML mutant Bcr-Abl [±] T315I [±] and preempts [±] in vitro [±] resistance when combined with nilotinib or dasatinib. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5507-5512.	7.1	84
82	PDB-Dev: a Prototype System for Depositing Integrative/Hybrid Structural Models. <i>Structure</i> , 2017, 25, 1317-1318.	3.3	84
83	[±] RCSB [±] Protein Data Bank: Celebrating 50 [±] years of the [±] PDB [±] with new tools for understanding and visualizing biological macromolecules in [±] 3D [±] . <i>Protein Science</i> , 2022, 31, 187-208.	7.6	84
84	[10] Dynamic light scattering in evaluating crystallizability of macromolecules. <i>Methods in Enzymology</i> , 1997, 276, 157-166.	1.0	80
85	Cas5d processes pre-crRNA and is a member of a larger family of CRISPR RNA endonucleases. <i>Rna</i> , 2012, 18, 2020-2028.	3.5	80
86	X-Ray Structure of a Rex-Family Repressor/NADH Complex Insights into the Mechanism of Redox Sensing. <i>Structure</i> , 2005, 13, 43-54.	3.3	78
87	X-ray Structure of Translation Initiation Factor eIF2 [±] . <i>Journal of Biological Chemistry</i> , 2004, 279, 10634-10642.	3.4	73
88	X-ray crystal structure of the B component of Hemolysin BL from [±] Bacillus cereus [±] . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 534-540.	2.6	73
89	Engaging the ribosome: universal IFs of translation. <i>Trends in Biochemical Sciences</i> , 2001, 26, 705-709.	7.5	71
90	Crystal structures of ribosome anti-association factor IF6. <i>Nature Structural Biology</i> , 2000, 7, 1156-1164.	9.7	70

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91	Integrative Structureâ€“Function Mapping of the Nucleoporin Nup133 Suggests a Conserved Mechanism for Membrane Anchoring of the Nuclear Pore Complex. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2911-2926.	3.8	67
92	She2p Is a Novel RNA Binding Protein with a Basic Helical Hairpin Motif. <i>Cell</i> , 2004, 119, 491-502.	28.9	66
93	RCSB Protein Data Bank: A Resource for Chemical, Biochemical, and Structural Explorations of Large and Small Biomolecules. <i>Journal of Chemical Education</i> , 2016, 93, 569-575.	2.3	66
94	How Structural Biologists and the Protein Data Bank Contributed to Recent FDA New Drug Approvals. <i>Structure</i> , 2019, 27, 211-217.	3.3	65
95	STRUCTURING THEUNIVERSE OFPROTEINS. <i>Annual Review of Genomics and Human Genetics</i> , 2002, 3, 243-262.	6.2	62
96	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. <i>Structure</i> , 2006, 14, 1211-1217.	3.3	60
97	Investigation of the Roles of Catalytic Residues in Serotonin N-Acetyltransferase. <i>Journal of Biological Chemistry</i> , 2002, 277, 18118-18126.	3.4	59
98	Protein-RNA and Protein-Protein Recognition by Dual KH1/2 Domains of the Neuronal Splicing Factor Nova-1. <i>Structure</i> , 2011, 19, 930-944.	3.3	59
99	Contributions to the NIH-NIGMS Protein Structure Initiative from the PSI Production Centers. <i>Structure</i> , 2008, 16, 5-11.	3.3	58
100	Cocystal Structures of Diaminopimelate Decarboxylase. <i>Structure</i> , 2002, 10, 1499-1508.	3.3	57
101	Two Structurally Atypical HEAT Domains in the C-Terminal Portion of Human eIF4G Support Binding to eIF4A and Mnk1. <i>Structure</i> , 2006, 14, 913-923.	3.3	56
102	High-throughput Limited Proteolysis/Mass Spectrometry for Protein Domain Elucidation. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 129-134.	1.2	55
103	Impact of genetic variation on three dimensional structure and function of proteins. <i>PLoS ONE</i> , 2017, 12, e0171355.	2.5	55
104	X-ray crystallographic studies of serotonin N-acetyltransferase catalysis and inhibition. <i>Journal of Molecular Biology</i> , 2002, 317, 215-224.	4.2	54
105	Crystal structure of trehalose-6-phosphate phosphatase-related protein: Biochemical and biological implications. <i>Protein Science</i> , 2006, 15, 1735-1744.	7.6	54
106	Crystal structure of theStreptococcus pneumoniae phosphomevalonate kinase, a member of the GHMP kinase superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 568-571.	2.6	53
107	Structure, Dynamics, Evolution, and Function of a Major Scaffold Component in the Nuclear Pore Complex. <i>Structure</i> , 2013, 21, 560-571.	3.3	53
108	Histone-like transcription factors in eukaryotes. <i>Current Opinion in Structural Biology</i> , 1997, 7, 94-102.	5.7	49

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109	The Protein Data Bank Archive. <i>Methods in Molecular Biology</i> , 2021, 2305, 3-21.	0.9	49
110	Recognizing DNA in the library. <i>Nature</i> , 2000, 404, 715-717.	27.8	48
111	New York-Structural GenomiX Research Consortium (NYSGXRC): A Large Scale Center for the Protein Structure Initiative. <i>Journal of Structural and Functional Genomics</i> , 2005, 6, 225-232.	1.2	48
112	Molecular mechanism of recruitment of TFIIIF- associating RNA polymerase C-terminal domain phosphatase (FCP1) by transcription factor IIF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2296-2299.	7.1	46
113	Announcing mandatory submission of PDBx/mmCIF format files for crystallographic depositions to the Protein Data Bank (PDB). <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 451-454.	2.3	46
114	The Kinetic Mechanism of Phosphomevalonate Kinase. <i>Journal of Biological Chemistry</i> , 2003, 278, 4510-4515.	3.4	45
115	Structural basis for activation of the therapeutic L-nucleoside analogs 3TC and troxacitabine by human deoxycytidine kinase. <i>Nucleic Acids Research</i> , 2006, 35, 186-192.	14.5	45
116	Worldwide Protein Data Bank biocuration supporting open access to high-quality 3D structural biology data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018, 2018, .	3.0	45
117	BioJava 5: A community driven open-source bioinformatics library. <i>PLoS Computational Biology</i> , 2019, 15, e1006791.	3.2	44
118	<scp>PDB</scp>â€101: Educational resources supporting molecular explorations through biology and medicine. <i>Protein Science</i> , 2022, 31, 129-140.	7.6	43
119	Catalytic Mechanism and Three-Dimensional Structure of Adenine Deaminase[,]. <i>Biochemistry</i> , 2011, 50, 1917-1927.	2.5	42
120	Structural Variation in Bacterial Glyoxalase I Enzymes. <i>Journal of Biological Chemistry</i> , 2011, 286, 38367-38374.	3.4	42
121	Real time structural search of the Protein Data Bank. <i>PLoS Computational Biology</i> , 2020, 16, e1007970.	3.2	42
122	Structure determination of an FMN reductase from <i>Pseudomonas aeruginosa</i> PAO1 using sulfur anomalous signal. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 383-391.	2.5	41
123	Characterization of metalloproteins by high-throughput X-ray absorption spectroscopy. <i>Genome Research</i> , 2011, 21, 898-907.	5.5	41
124	RCSB Protein Data Bank: improved annotation, search and visualization of membrane protein structures archived in the PDB. <i>Bioinformatics</i> , 2022, 38, 1452-1454.	4.1	41
125	Crystal Structure of Shikimate 5-Dehydrogenase (SDH) Bound to NADP. <i>Structure</i> , 2003, 11, 1005-1013.	3.3	40
126	Re-refinement of the X-ray Crystal Structure of Bovine Lens Leucine Aminopeptidase Complexed with Bestatin. <i>Journal of Molecular Biology</i> , 1993, 230, 722-724.	4.2	39

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127	PDBx/mmCIF Ecosystem: Foundational Semantic Tools for Structural Biology. <i>Journal of Molecular Biology</i> , 2022, 434, 167599.	4.2	39
128	DNA-binding motifs from eukaryotic transcription factors. <i>Current Opinion in Structural Biology</i> , 1994, 4, 3-11.	5.7	38
129	Structural genomics of proteins from conserved biochemical pathways and processes. <i>Current Opinion in Structural Biology</i> , 2002, 12, 383-391.	5.7	38
130	TATA Box Mimicry by TFIID. <i>Cell</i> , 1998, 94, 551-553.	28.9	36
131	Design and proof of concept for targeted phage-based COVID-19 vaccination strategies with a streamlined cold-free supply chain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	35
132	The Hunt for 8-Oxoguanine Deaminase. <i>Journal of the American Chemical Society</i> , 2010, 132, 1762-1763.	13.7	34
133	Transcription factor complexes. <i>Current Opinion in Structural Biology</i> , 2002, 12, 225-230.	5.7	33
134	High Throughput Protein Production and Crystallization at NYSGXRC. <i>Methods in Molecular Biology</i> , 2008, 426, 561-575.	0.9	33
135	Blocking UV-induced eIF2 γ Phosphorylation with Small Molecule Inhibitors of GCN2. <i>Chemical Biology and Drug Design</i> , 2009, 74, 57-67.	3.2	32
136	Structure and Catalytic Mechanism of LigI: Insight into the Amidohydrolase Enzymes of cog3618 and Lignin Degradation. <i>Biochemistry</i> , 2012, 51, 3497-3507.	2.5	32
137	Crystal structure of the <i>Escherichia coli</i> shikimate kinase I (AroK) that confers sensitivity to mecillinam. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 558-562.	2.6	31
138	Evolution of the SARS-CoV-2 proteome in three dimensions (3D) during the first 6 months of the COVID-19 pandemic. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1054-1080.	2.6	31
139	Structural and Functional Studies of Fatty Acyl Adenylate Ligases from <i>E. coli</i> and <i>L. pneumophila</i> . <i>Journal of Molecular Biology</i> , 2011, 406, 313-324.	4.2	29
140	Loss of quaternary structure is associated with rapid sequence divergence in the OSBS family. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 8535-8540.	7.1	29
141	Crystal structure of the <i>Escherichia coli</i> glucose-inhibited division protein B (GidB) reveals a methyltransferase fold. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 563-567.	2.6	28
142	Structural Analysis of a Ternary Complex of Allantoate Amidohydrolase from <i>Escherichia coli</i> Reveals its Mechanics. <i>Journal of Molecular Biology</i> , 2007, 368, 450-463.	4.2	28
143	Rapid-access, high-throughput synchrotron crystallography for drug discovery. <i>Trends in Pharmacological Sciences</i> , 2012, 33, 261-267.	8.7	28
144	The archiving and dissemination of biological structure data. <i>Current Opinion in Structural Biology</i> , 2016, 40, 17-22.	5.7	28

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145	Multivariate Analyses of Quality Metrics for Crystal Structures in the PDB Archive. <i>Structure</i> , 2017, 25, 458-468.	3.3	28
146	Enhanced validation of small-molecule ligands and carbohydrates in the Protein Data Bank. <i>Structure</i> , 2021, 29, 393-400.e1.	3.3	28
147	A Novel Acquired Exon 20 EGFR M766Q Mutation in Lung Adenocarcinoma Mediates Osimertinib Resistance but is Sensitive to Neratinib and Poziotinib. <i>Journal of Thoracic Oncology</i> , 2019, 14, 1982-1988.	1.1	27
148	Structural Bases of PAS Domain-regulated Kinase (PASK) Activation in the Absence of Activation Loop Phosphorylation. <i>Journal of Biological Chemistry</i> , 2010, 285, 41034-41043.	3.4	26
149	Target selection and annotation for the structural genomics of the amidohydrolase and enolase superfamilies. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 107-125.	1.2	25
150	Crystal structure of the <i>Escherichia coli</i> SbmC protein that protects cells from the DNA replication inhibitor microcin B17. <i>Proteins: Structure, Function and Bioinformatics</i> , 2002, 47, 403-407.	2.6	24
151	Enzymatic Deamination of the Epigenetic Base <i>N</i> -6-Methyladenine. <i>Journal of the American Chemical Society</i> , 2011, 133, 2080-2083.	13.7	24
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